



Nucleotide

Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Book
Search	Nucleotide		for					
		Limits	Preview/Index		History	Clipboard	Details	
Display	default	Show: 20	Send to	File		Get Subsequence	Features	Links
1: AY237642. Erwinia pyrifoliae [gi:33359597]								
LOCUS	AY237642	1353 bp	DNA	linear	BCT	01-MAR-2004		
DEFINITION	Erwinia pyrifoliae HrpW (hrpW) gene, complete cds.							
ACCESSION	AY237642							
VERSION	AY237642.1	GI:33359597						
KEYWORDS								
SOURCE	Erwinia pyrifoliae							
ORGANISM	Erwinia pyrifoliae							
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Erwinia.								
REFERENCE	1 (bases 1 to 1353)							
AUTHORS	Shrestha,R., Baek,S.J., Bae,H.N., Cho,J.M., Park,D.H., Hwang,I.K., Hur,J.H. and Lim,C.K.							
TITLE	Molecular characterization hrp genes cluster of Erwinia pyrifoliae and expression of hrpEp encoding elicitor of the hypersensitive response							
JOURNAL	Unpublished							
REFERENCE	2 (bases 1 to 1353)							
AUTHORS	Shrestha,R., Hur,J.H. and Lim,C.K.							
TITLE	Direct Submission							
JOURNAL	Submitted (17-FEB-2003) Biological Environment, Gangwon National University, Hyo-ja 2dong, Chunchon, Gangwon 200-701, Republic of Korea							
FEATURES	Location/Qualifiers							
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CDS	1..1353							
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ORIGIN	1 atgtcagtttc ttacgcttaa catcatgtatc ccgtcctcgcc aggggctatt caagcccgcc 61 gaagacaacg gacttagtgg tcaaaaataca aattcaacac aggggcagca ccccatcgat							

61 gaagacaacg gacttagtgg tcaaaaataca aattcagcac aggggcagca ccccatcgat

CLUSTAL W (1.82) multiple sequence alignment

Eamylovora_HrpW	ATGTCAATTCTTACGCTAACACAATACCTCGTCTCGCCGGTCTGTTCCAGTCGGG 6
Epyrifoliae_HrpW	ATGTCAGTTCTTACGCTAACATCAGTATCCCGTCTCGCAGGGGCTATTCAAGCCC 6
***** * *****	
Eamylovora_HrpW	GGGGACAACGGGCTTGGTGGTCATAATGCAAATTCTGCCTGGGCAACAACCCATCGAT 1
Epyrifoliae_HrpW	GAAGACAACGGACTTAGTGGTAAAATACAAATTACAGCACAGGGGCAAGCCCCATCGAT 1
* * *****	
Eamylovora_HrpW	CGGCAAACCATTGAGCAAATGGCTCAATTATTGGCGGAACTGTTAAAGTCACTGCTATCG 1
Epyrifoliae_HrpW	CGGCAAACCATTGAGCAAATGGCGCAATTATTGGGAGAACTGTTAAAGCGCTGCTATCG 1

Eamylovora_HrpW	CCACAATCAGGTAATGCGCAACCGGAGGCCGGTGCACGACTACAGGAGTTGGT 2
Epyrifoliae_HrpW	CCACAGGCAGATAATGCAGCA-----GCAGGTAGCAATGACCAACGGAGTGGG 2

Eamylovora_HrpW	AACGCTGGCGGCCTGAACGGACGAAAGGCACAGCAGGAACCACTCCGAGTGTGACAGT 3
Epyrifoliae_HrpW	AACGCTGGCGGCCTGACGGGAAATGGCGCAGCAGGGACTACCCCGAGTGTGCAAC 2

Eamylovora_HrpW	CAGAACATGCTGAGTGAGATGGCAACAAACGGCTGGATCAGGCCATCACGCCCGATGGC 3
Epyrifoliae_HrpW	CAGACAATGCTGGGTGAGATGGCAATAACGGGCTGGATCAGGCCATCACGCCCGATGGC 3

Eamylovora_HrpW	CAGGGCGGCGGGCAGATCGGCATAATCCTTACTGAAAGCCATGCTGAAGCTTATTGCA 4
Epyrifoliae_HrpW	CAGGGCGGCGGGCAGATCGGCATAATCCTTACTGAAAGCCATGCTAAAGCTTATCGC 4

Eamylovora_HrpW	CGCATGATGGACGGCAAAGCGATCAGTTGGCAACCTGGTACGGCAACAACAGTGC 4
Epyrifoliae_HrpW	CGCATGATGGACGGCAAAGTGACACGTTGGCCAGCCGGATCCGGCAATAATGATGCG 4

Eamylovora_HrpW	TCTTCCGGTACTTCTTCATCTGGCGTTCCCTTTAACGAT-----CTAT 5
Epyrifoliae_HrpW	TCTTCCGGCCCTTCTCGGCGGGGAATTATCCTGCCAGCAACGCGTCTCTGGCTTCT 5

Eamylovora_HrpW	CAGGGGGGAAGGCCCT-TCCGGCAACTCCCTCCGGCAACTACTCTCCCGTCAGTACC 5
Epyrifoliae_HrpW	CTCGGGGGAAAGTTCTCTGTAGGTAAAGCGTCTCTGGCGCACATCTCCACCAATTCC 5
* *****	
Eamylovora_HrpW	TTCTCACCCCCATCCACGCCAACGCCCTACCTCACCGCTTGATTTCCCTCTTCTCCC 6
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Eamylovora_HrpW	ACCAAAGCAGCGGGGGCAGCACGCCGTAACCGATCATCTGACCTGTTGGTAGCGCG 7
Epyrifoliae_HrpW	ACCAAGCGGTGCCGGGGCAGCACGCCGGTACCGATCATGCTGACCTGTCGGCAGTACC 7

Eamylovora_HrpW	GGCATGGGGCCGGAAATTGGTGGCTTCACCGCAGCGCCGGCTAACATGACGGTGCTG 7
Epyrifoliae_HrpW	GGCGTGGGGCCGGAAATTGGTGGCTTACCGCAGCGCCGGCTAACCCGACTGTGCTG 7

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Epyrifoliae_HrpW	GAAGACGGTGCCAGCCTGAAAAACGTACCATGGCGATGGGCGGATGGCATT CAT	9

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Epyrifoliae_HrpW	CTTTACGGTGATGCCAAAATAGACAATCTGCACGTCAACAGTGGAGAGGACCGC GATA	1

Eamylovora_HrpW	ACCGTTAACGCCAACAGCGCGGGCAAAAATCCACGTTGAAATCACTAACAGTC CTTTC	1
Epyrifoliae_HrpW	ACCGTTAACGCCAACAGCGCTGGCAAAAATCTCACGTTGACATCAACAGTC CTTTT	1

Eamylovora_HrpW	GAGCACGCCTCTGACAAGATCCTGCAGCTGAATGCCATACTAACCTGAGCGTT GACAAC	1
Epyrifoliae_HrpW	GAGCACGCCTCTGACAAGATCCTGCAGCTGAATGCTGATACCACCCCTGAA CGTTGACAAC	1

Eamylovora_HrpW	GTGAAGGCCAAAGACTTGGTACTTTGTACGCACTAACGGCGGTCAACAGGGTAA CTGG	1
Epyrifoliae_HrpW	GTGAAGGCCAAAGACTTGGTACTTCGTACGCACTAACGGAGGTCAACAGGGTAA CTGG	1

Eamylovora_HrpW	GATCTGAATCTGAGCCATATCAGCGCAGAAGACGGTAAGTCTCGTCGTTAAAAG CGAT	1
Epyrifoliae_HrpW	GATCTGAATCTGAGCCATATCAGCGCAGAGAACGGTAAATTCTCGTCGTTAAAAG CGAT	1

Eamylovora_HrpW	AGCGAGGGGCTAAACGTCAATACCACTGATATCTCACTGGGTGATGTTGAAAACC ACTAC	1
Epyrifoliae_HrpW	AGCGAGGGGCTAAACGTCAATACCACTGATATCTCACTGGCAACGTTGAAAACC ACTAT	1

Eamylovora_HrpW	AAAGTGCCGATGTCCGCCAACCTGAAGGTGGCTGAATGA 1344	
Epyrifoliae_HrpW	AAAGTGCCGATGTCCGCCAACCTGAAGGTGGCTAAATGA 1353	

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: Eamylovora_HrpW 1344 bp

Sequence 2: Epyrifoliae_HrpW 1353 bp

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 86

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-2]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:22855

Alignment Score 8504

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-200]